



#12

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: LITTMAN, DAN R.
DENG, HONGKUI
ELLMEIER, WILFRIED
LANDAU, NATHANIEL R.
LIU, RONG
- (ii) TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
USES THEREOF
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: David A. Jackson, Esq.
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Floor
 - (C) CITY: Hackensack
 - (D) STATE: New Jersey
 - (E) COUNTRY: USA
 - (F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/734,221
 - (B) FILING DATE: 2000/12/11
 - (C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/666,020
 - (B) FILING DATE: 19-JUN-1996
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/227,319
 - (B) FILING DATE: 13-APR-1994
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Jackson Esq., David A.
 - (B) REGISTRATION NUMBER: 26,742
 - (C) REFERENCE/DOCKET NUMBER: 1049-1-004 N2
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 201-487-5800
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCGGATCCG GTGGAACAAG ATGGATTAT

29

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTCGTCGACA TGTGCACAAC TCTGACTG

28

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGATTATC AAGTGTCAAG TCCAATCTAT GACATCAATT ATTATACATC GGAGCCCTGC

60

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asp	Tyr	Gln	Val	Ser	Ser	Pro	Ile	Tyr	Asp	Ile	Asn	Tyr	Tyr	Thr
1				5					10					15	
Ser Glu Pro Cys Gln Lys															
20															

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGATTATC AAGTGTCAAG TCCAATCTAT GACATCAATT ATCCATACGA TGTTCCAGAT	60
TATGCTTCGG AGCCCTGCCA AAAA	84

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Pro Tyr
1 5 10 15

Asp Val Pro Asp Tyr Ala Ser Glu Pro Cys Gln Lys
20 25

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotides"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATCAATTATC CATACGATGT TCCAGATTAT GCTTCGGAGC CCTGCCAAAA A

51

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotides"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCAGGATCCA CCATGGATTA TCAAGTGTCA AGTCCAATCT ATGACATCAA TTATCCATAC
GAT

60

63

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCATACGATG TTCCAGATTA TGCT

24

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TATCCATACG ATGTTCCAGA TTATGCTTCG

30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3383 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGAAGAGCTG	AGACATCCGT	TCCCCTACAA	GAAACTCTCC	CCGGGTGGAA	CAAGATGGAT	60
TATCAAGTGT	CAAGTCCAAT	CTATGACATC	AATTATTATA	CATCGGAGCC	CTGCCAAAAA	120
ATCAATGTGA	AGCAAATCGC	AGCCCGCCTC	CTGCCTCCGC	TCTACTCACT	GGTGTTCATC	180
TTTGGTTTTG	TGGGCAACAT	GCTGGTCATC	CTCATCCTGA	TAAACTGCAA	AAGGCTGAAG	240
AGCATGACTG	ACATCTACCT	GCTCAACCTG	GCCATCTCTG	ACCTGTTTTT	CCTTCTTACT	300
GTCCCCTTCT	GGGCTCACTA	TGCTGCCGCC	CAGTGGGACT	TTGGAAATAC	AATGTGTCAA	360
CTCTTGACAG	GGCTCTATTT	TATAGGCTTC	TTCTCTGGAA	TCTTCTTCAT	CATCCTCCTG	420
ACAATCGATA	GGTACCTGGC	TGTCGTCCAT	GCTGTGTTTG	CTTTAAAAGC	CAGGACGGTC	480
ACCTTTGGGG	TGGTGACAAG	TGTGATCACT	TGGGTGGTGG	CTGTGTTTGC	GTCTCTCCCA	540
GGAATCATCT	TTACCAGATC	TCAAAAAGAA	GGTCTTCATT	ACACCTGCAG	CTCTCATTTT	600
CCATCAGTCT	AGTATCAATT	CTGGAAGAAT	TTCCAGACAT	TAAAGATAGT	CATCTTGGGG	660
CTGGTCCTGC	CGCTGCTTGT	CATGGTCATC	TGCTACTCGG	GAATCCTAAA	AACTCTGCTT	720
CGGTGTGCGA	ATGAGAAGAA	GAGGCACAGG	GCTGTGAGGC	TTATCTTCAC	CATCATGATT	780
GTTTATTTTC	TCTTCTGGGC	TCCCTACAAC	ATTGTCCTTC	TCCTGAACAC	CTTCCAGGAA	840
TTCTTTGGCC	TGAATAATTG	CAGTAGCTCT	AACAGGTTGG	ACCAAGCTAT	GCAGGTGACA	900
GAGACTCTTG	GGATGACGCA	CTGCTGCATC	AACCCCATCA	TCTATGCCTT	TGTCGGGGAG	960
AAGTTCAGAA	ACTACCTCTT	AGTCTTCTTC	CAAAAGCACA	TTGCCAAACG	CTTCTGCAAA	1020
TGCTGTTCTA	TTTTCCAGCA	AGAGGCTCCC	GAGCGAGCAA	GCTCAGTTTA	CACCCGATCC	1080
ACTGGGGAGC	AGGAAATATC	TGTGGGCTTG	TGACACGGAC	TCAAGTGGGC	TGGTGACCCA	1140
GTCAGAGTTG	TGCACATGGC	TTAGTTTTCA	TACACAGCCT	GGGCTGGGGG	TGGGGTGGGA	1200
GAGGTCTTTT	TTAAAAGGAA	GTTACTGTTA	TAGAGGGTCT	AAGATTCATC	CATTTATTTG	1260
GCATCTGTTT	AAAGTAGATT	AGATCTTTTA	AGCCCATCAA	TTATAGAAAAG	CCAAATCAAA	1320
ATATGTTGAT	GAAAAATAGC	AACCTTTTTA	TCTCCCCTTC	ACATGCATCA	AGTTATTGAC	1380
AAACTCTCCC	TTCACTCCGA	AAGTTCCTTA	TGTATATTTA	AAAGAAAGCC	TCAGAGAATT	1440
GCTGATTCTT	GAGTTTAGTG	ATCTGAACAG	AAATACCAAA	ATTATTTTCA	AAATGTACAA	1500
CTTTTTACCT	AGTACAAGGC	AACATATAGG	TTGTAAATGT	GTTTAAAACA	GGTCTTTGTC	1560
TTGCTATGGG	GAGAAAAGAC	ATGAATATGA	TTAGTAAAGA	AATGACACTT	TTCATGTGTG	1620
ATTTCCCCTC	CAAGGTATGG	TTAATAAGTT	TCCTGACTT	AGAACCAGGC	GAGAGACTTG	1680
TGGCCTGGGA	GAGCTGGGGA	AGCTTCTTAA	ATGAGAAGGA	ATTTGAGTTG	GATCATCTAT	1740
TGCTGGCAAA	GACAGAAGCC	TCCTGCAAG	CACCTGCATG	GCAAGCTTGG	CTGTAGAAGG	1800
AGACAGAGCT	GGTTGGGAAG	ACATGGGGAG	GAAGGACAAG	GCTAGATCAT	GAAGAACCTT	1860
GACGGCATTG	CTCCGTCTAA	GTCATGAGCT	GAGCAGGGAG	ATCCTGGTTG	GTGTTGCAGA	1920
AGGTTTACTC	TGTGGCCAAA	GGAGGGTCAG	GAAGGATGAG	CATTTAGGGC	AAGGAGACCA	1980
CCAACAGCCC	TCAGGTCAGG	GTGAGGATGG	CCTCTGCTAA	GCTCAAGGCG	TGAGGATGGG	2040

AAGGAGGGAG	GTATTCGTAA	GGATGGGAAG	GAGGGAGGTA	TTCGTGCAGC	ATATGAGGAT	2100
GCAGAGTCAG	CAGAACTGGG	GTGGATTTGG	TTTGGAAGTG	AGGGTCAGAG	AGGAGTCAGA	2160
GAGAATCCCT	AGTCTTCAAG	CAGATTGGAG	AAACCCTTGA	AAAGACATCA	AGCACAGAAG	2220
GAGGAGGAGG	AGGTTTAGGT	CAAGAAGAAG	ATGGATTGGT	GTAAAAGGAT	GGGTCTGGTT	2280
TGCAGAGCTT	GAACACAGTC	TCACCCAGAC	TCCAGGCTGT	CTTTCAGTGA	ATGCTTCTGA	2340
CTTCATAGAT	TTCCTTCCCA	TCCCAGCTGA	AATACTGAGG	GGTCTCCAGG	AGGAGACTAG	2400
ATTTATGAAT	ACACGAGGTA	TGAGGTCTAG	GAACATACTT	CAGCTCACAC	ATGAGATCTA	2460
GGTGAGGATT	GATTACCTAG	TAGTCATTTT	ATGGGTTGTT	GGGAGGATTC	TATGAGGCAA	2520
CCACAGGCAG	CATTTAGCAC	ATACTACACA	TTCAATAAGC	ATCAAACCTCT	TAGTTACTCA	2580
TTCAGGGATA	GCACTGAGCA	AAGCATTGAG	CAAAGGGGTC	CCATATAGGT	GAGGGAAGCC	2640
TGAAAAACTA	AGATGCTGCC	TGCCCAGTGC	ACACAAGTGT	AGGTATCATT	TTCTGCATTT	2700
AACCGTCAAT	AGGCAAAGGG	GGGAAGGGAC	ATATTCATTT	GGAAATAAGC	TGCCTTGAGC	2760
CTTAAAACCC	ACAAAAGTAC	AATTTACCAG	CCTCCGTATT	TCAGACTGAA	TGGGGGTGGG	2820
GGGGGCGCCT	TAGGTACTTA	TTCCAGATGC	CTTCTCCAGA	CAAACCAGAA	GCAACAGAAA	2880
AAATCGTCTC	TCCCTCCCTT	TGAAATGAAT	ATACCCCTTA	GTGTTTGGGT	ATATTCATTT	2940
CAAAGGGAGA	GAGAGAGGTT	TTTTTCTGTT	CTTTCTCATA	TGATTGTGCA	CATACTTGAG	3000
ACTGTTTTGA	ATTTGGGGGA	TGGCTAAAAC	CATCATAGTA	CAGGTAAGGT	GAGGGAATAG	3060
TAAGTGGTGA	GAATACTCA	GGGAATGAAG	GTGTCAGAAT	AATAAGAGGT	GCTACTGACT	3120
TTCTCAGCCT	CTGAATATGA	ACGGTGAGCA	TTGTGGCTGT	CAGCAGGAAG	CAACGAAGGG	3180
AAATGTCTTT	CCTTTTGCTC	TTAAGTTGTG	GAGAGTGCAA	CAGTAGCATA	GGACCCTACC	3240
CTCTGGGCCA	AGTCAAAGAC	ATTCTGACAT	CTTAGTATTT	GCATATTCTT	ATGTATGTGA	3300
AAGTTACAAA	TTGCTTGAAA	GAAAATATGC	ATCTAATAAA	AAACACCTTC	TAAAATAAAA	3360
AAAAAAAAAA	AAAAAAAAAA	AAA				3383

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Asp	Tyr	Gln	Val	Ser	Ser	Pro	Ile	Tyr	Asp	Ile	Asn	Tyr	Tyr	Thr
1				5					10					15	
Ser	Glu	Pro	Cys	Gln	Lys	Ile	Asn	Val	Lys	Gln	Ile	Ala	Ala	Arg	Leu
			20					25					30		
Leu	Pro	Pro	Leu	Tyr	Ser	Leu	Val	Phe	Ile	Phe	Gly	Phe	Val	Gly	Asn
			35				40					45			
Met	Leu	Val	Ile	Leu	Ile	Leu	Ile	Asn	Cys	Lys	Arg	Leu	Lys	Ser	Met
		50				55					60				
Thr	Asp	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Leu	Phe	Phe	Leu
	65					70				75					80
Leu	Thr	Val	Pro	Phe	Trp	Ala	His	Tyr	Ala	Ala	Ala	Gln	Trp	Asp	Phe

85

90

95

Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
 100 105 110

Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
 115 120 125

Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
 130 135 140

Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
 145 150 155 160

Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
 165 170 175

Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
 180 185 190

Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
 195 200 205

Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
 210 215 220

Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
 225 230 235 240

Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
 245 250 255

Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
 260 265 270

Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
 275 280 285

His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
 290 295 300

Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
 305 310 315 320

Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
 325 330 335

Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
 340 345 350